

-1/5-

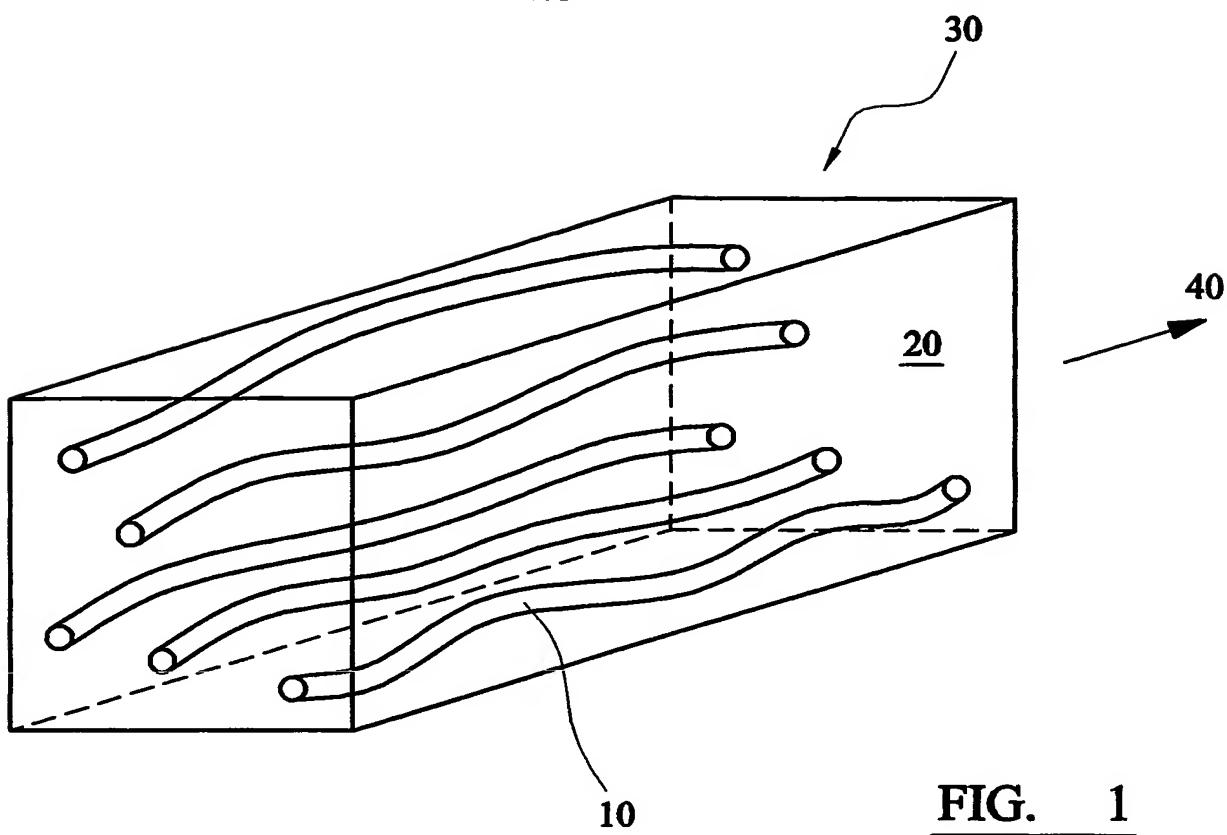


FIG. 1

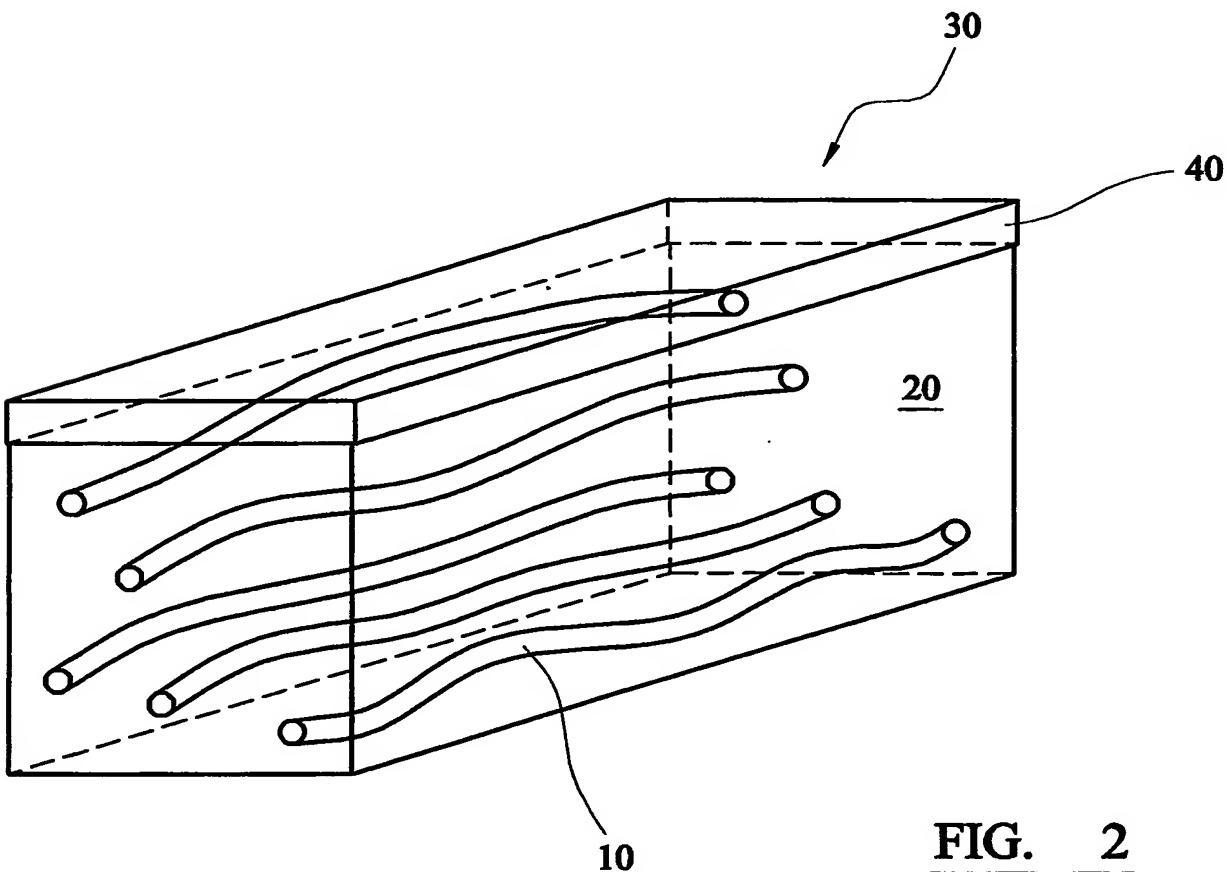


FIG. 2

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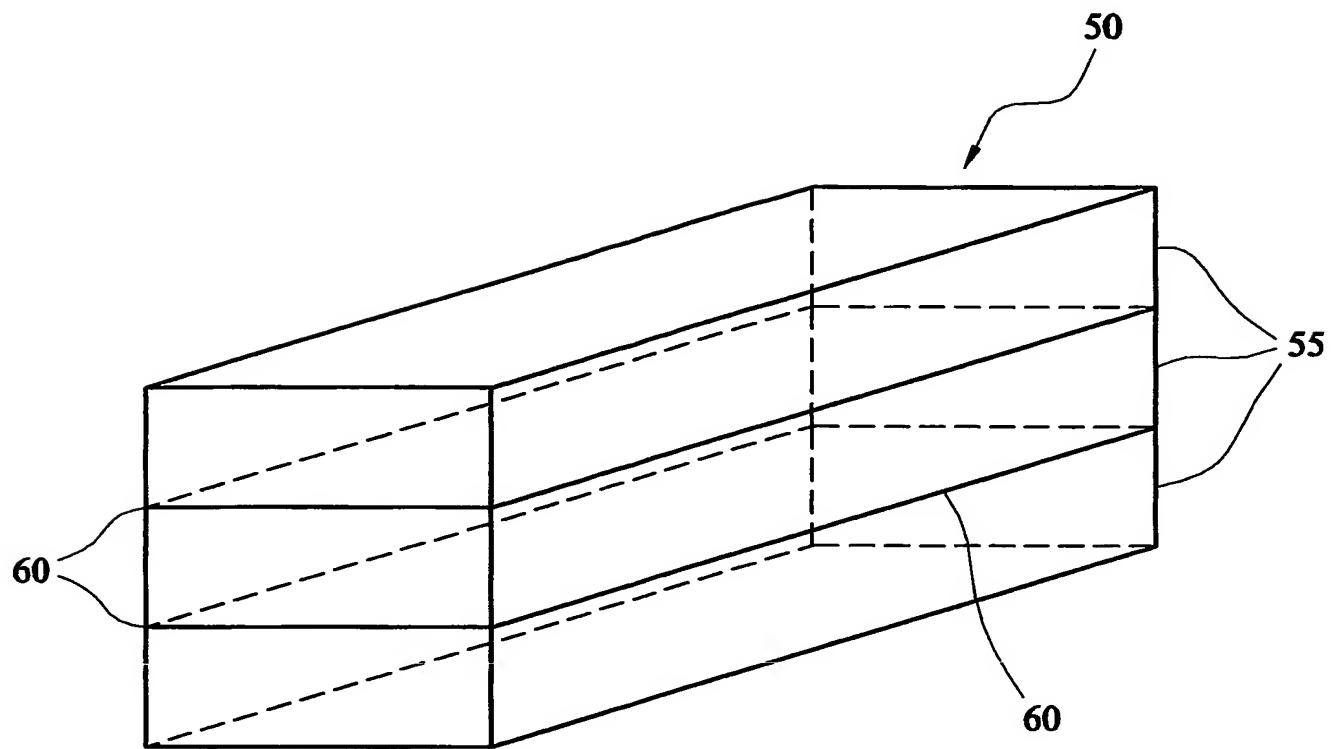


FIG. 3

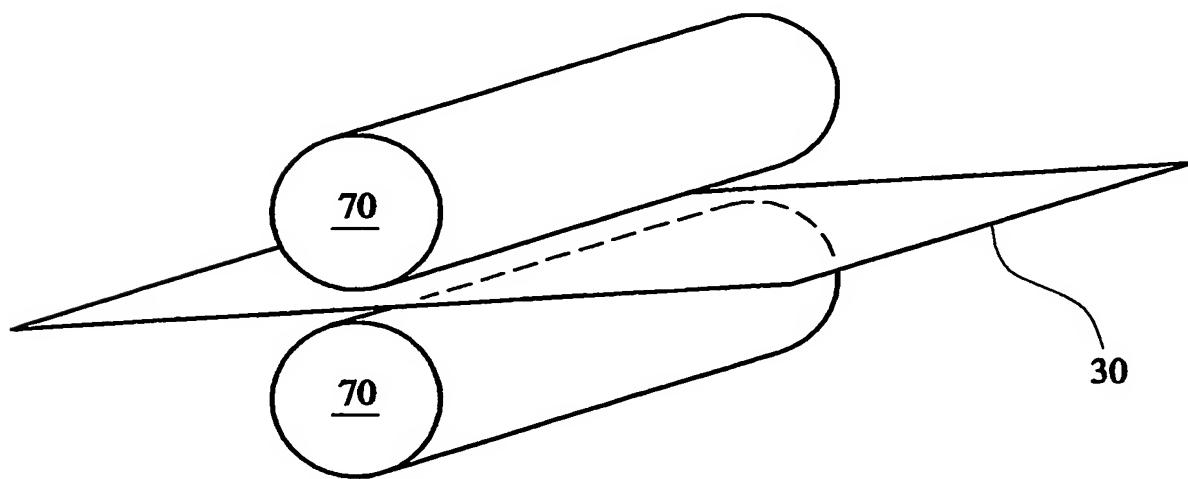


FIG. 4

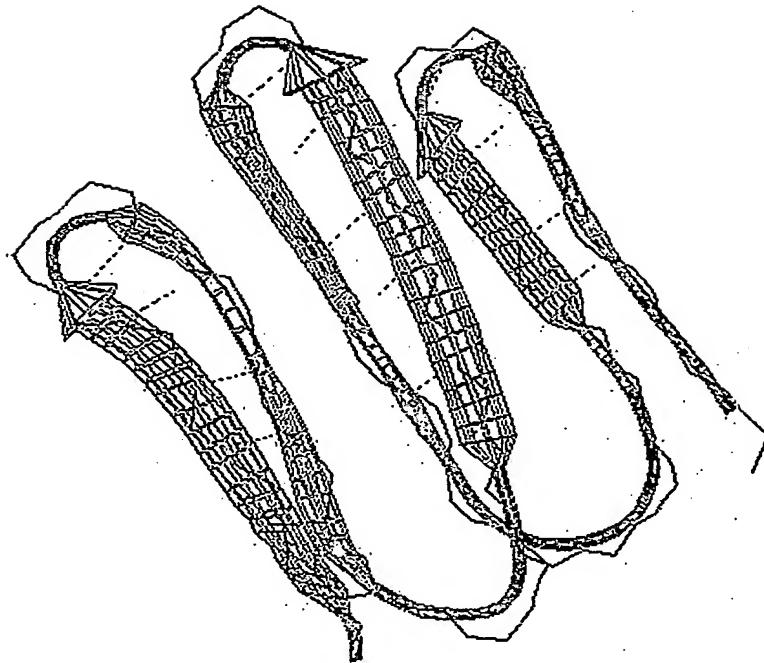
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Consensus repeat structure of sericin precursor protein

No. of Repeats	Total Score	Length	Diagonal	BW-From	BW-To	Level
7	529.97	35	35	317	351	1
131-	164 (46.31/ 7.35)	SSSSSSSTeess....	SSSR..	AASSTDASSNTDSNSNSA		
165-	202 (82.44/20.60)	GSSTS	GG..	RRTYGYSSNSRDGSV	STGSSNTDSNSNSA	
203-	240 (83.27/20.91)	GSSTS	GG..	SSTYGYSSNSRDGSV	STTGSSNTDSNSNSV	
241-	278 (68.12/15.35)	GSRRS	GG..	SSSHEDSSK	RDENVTIGSSNTDSNSNSV	
279-	316 (82.44/20.60)	GSSTS	GG..	RRTYGYSSNSRDGSV	SSSTGSSNTDSNSNSV	
317-	354 (84.15/21.23)	GSSTS	GG..	SSTYGYSSNSRDGSV	SSSTGSSNTDSNSNSA	
355-	389 (83.23/20.90)	GSSTE	GG..	SSTYGYSSNSHDGSV	SSSTGSSNTDSNS	

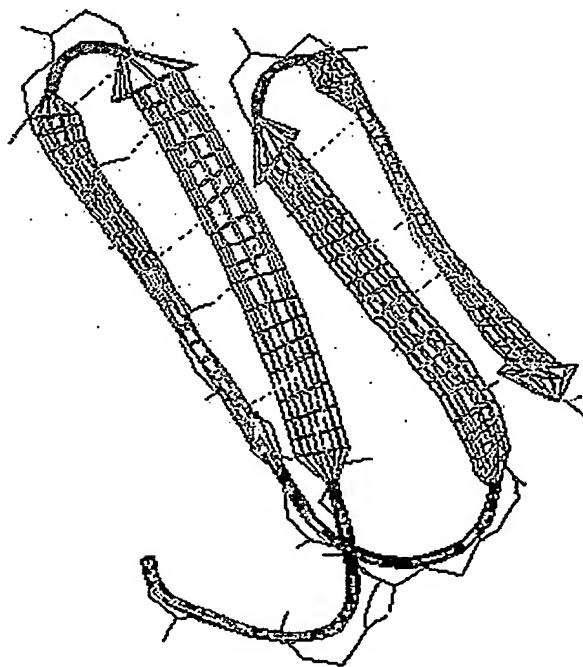
FIG. 5

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Ice nucleation protein (inaz) from the published PDB file

FIG. 6



Swiss model for consensus sequence of sericin precursor protein using
inaz as a template

FIG. 7

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The best LALIGN alignment of sericin precursor protein with INAC.

24.4% identity in 336 aa overlap; score: 265 E(10,000): 4.9e-16

	500	510	520	530	540	550
INAZ	STGTAGADSSLIAGYGSTQTSGSESSLTAGYGSTQTAREGSTLTAGYGSTGTAGADSSLI
serici	SAGAHRAKSVEQSQDKSKYTAGPSEGVTSGRSQNYKDSKQAIISGGTKSSNSNVQSDEKS

620	630	640	650	660	670	
INAZ	SFIIAGY---GSTQTAGHKSILTAGYGSTQTARDGSIDLIAKYGSTGTAGS---GSSLIA					
...	
serici	TYGYSSNSRDGSVSSTGSSNTDSNNSNAGSSTSGGSSTYGYSSNSRDGSVSTTGSSSNT					
	180	190	200	210	220	230

	680	690	700	710	720	730	
INAZ	GYGSTQTASYRSMLTAGYGSTQTAREHSDLVTGYGSTSTAGSNSSLIAGYGSTQTAGFKS::.....::.....::.....::.....::.....::.....::.....::.....::.....::					
serici	DSNSNSVGSRRSGGSSSHEDSSKSRDENVSTTGSSSNTDSNSNSVGSSTSGGRRTYGYSS	240	250	260	270	280	290

FIG. 8